

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/S27,571A
Source: IFWO
Date Processed by STIC: 8/22/06

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IFWO

RAW SEQUENCE LISTING

DATE: 08/22/2006

PATENT APPLICATION: US/10/527,571A

TIME: 11:14:39

Input Set : N:\RJAVED\10527571.txt

Output Set: N:\CRF4\08222006\J527571A.raw

(Pg. 6)

3 <110> APPLICANT: Syngenta Participations AG
 4 Stam, Lynn
 5 Kamdar, Kim
 6 Spana, Eric
 7 Bachmann, Jane
 9 <120> TITLE OF INVENTION: Nucleic Acid Sequences from Drosophila Melanogaster that
 Encode Proteins
 10 Essential for Viability and Uses Thereof
 12 <130> FILE REFERENCE: 70131USPCT
 14 <140> CURRENT APPLICATION NUMBER: US/10/527,571A
 15 <141> CURRENT FILING DATE: 2005-03-14
 17 <150> PRIOR APPLICATION NUMBER: 60/422,377
 18 <151> PRIOR FILING DATE: 2002-10-29
 20 <160> NUMBER OF SEQ ID NOS: 381
 22 <170> SOFTWARE: PatentIn version 3.1
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 27
 26 <212> TYPE: DNA
 27 <213> ORGANISM: artificial sequence
 29 <220> FEATURE:
 30 <221> NAME/KEY: misc_feature
 31 <222> LOCATION: (1)..(27)
 32 <223> OTHER INFORMATION: primer Plac4
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 36 actgtgcggt aggtcctggt cattggt 27
 39 <210> SEQ ID NO: 2
 40 <211> LENGTH: 24
 41 <212> TYPE: DNA
 42 <213> ORGANISM: artificial sequence
 44 <220> FEATURE:
 45 <221> NAME/KEY: misc_feature
 46 <222> LOCATION: (1)..(24)
 47 <223> OTHER INFORMATION: Primer Plac1
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 51 cacccaaggc tctgctccca caat 24
 54 <210> SEQ ID NO: 3
 55 <211> LENGTH: 23
 56 <212> TYPE: DNA
 57 <213> ORGANISM: artificial sequence
 59 <220> FEATURE:
 60 <221> NAME/KEY: misc_feature
 61 <222> LOCATION: (1)..(23)
 62 <223> OTHER INFORMATION: Primer Pry4
 65 <400> SEQUENCE: 3

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66 caatcatatc gctgtctcac tca                                     23
69 <210> SEQ ID NO: 4
70 <211> LENGTH: 26
71 <212> TYPE: DNA
72 <213> ORGANISM: artificial sequence
74 <220> FEATURE:
75 <221> NAME/KEY: misc_feature
76 <222> LOCATION: (1)..(26)
77 <223> OTHER INFORMATION: Primer Pry1
80 <400> SEQUENCE: 4
81 ccttagcatg tccgtgggggt ttgaat                                   26
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85 <211> LENGTH: 28
86 <212> TYPE: DNA
87 <213> ORGANISM: artificial sequence
89 <220> FEATURE:
90 <221> NAME/KEY: misc_feature
91 <222> LOCATION: (1)..(28)
92 <223> OTHER INFORMATION: Primer Pry2
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96 cttgccgacg ggaccacctt atgttatt                                   28
99 <210> SEQ ID NO: 6
100 <211> LENGTH: 19
101 <212> TYPE: DNA
102 <213> ORGANISM: artificial sequence
104 <220> FEATURE:
105 <221> NAME/KEY: misc_feature
106 <222> LOCATION: (1)..(19)
107 <223> OTHER INFORMATION: Primer Plw3-1
110 <400> SEQUENCE: 6
111 tgtcggcgctc atcaactcc                                           19
114 <210> SEQ ID NO: 7
115 <211> LENGTH: 29
116 <212> TYPE: DNA
117 <213> ORGANISM: artificial sequence
119 <220> FEATURE:
120 <221> NAME/KEY: misc_feature
121 <222> LOCATION: (1)..(29)
122 <223> OTHER INFORMATION: Primer Pwht1
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126 gtaacgctaa tcaactccgaa caggtcaca                               29
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130 <211> LENGTH: 25
131 <212> TYPE: DNA
132 <213> ORGANISM: artificial sequence
134 <220> FEATURE:
135 <221> NAME/KEY: misc_feature
136 <222> LOCATION: (1)..(25)
137 <223> OTHER INFORMATION: Primer Splac2

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140 <400> SEQUENCE: 8
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145 <211> LENGTH: 22
146 <212> TYPE: DNA
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151 <222> LOCATION: (1)..(22)
152 <223> OTHER INFORMATION: Primer Sp1
155 <400> SEQUENCE: 9
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160 <211> LENGTH: 24
161 <212> TYPE: DNA
162 <213> ORGANISM: artificial sequence
164 <220> FEATURE:
165 <221> NAME/KEY: misc_feature
166 <222> LOCATION: (1)..(24)
167 <223> OTHER INFORMATION: Primer Sp3
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174 <210> SEQ ID NO: 11
175 <211> LENGTH: 23
176 <212> TYPE: DNA
177 <213> ORGANISM: artificial sequence
179 <220> FEATURE:
180 <221> NAME/KEY: misc_feature
181 <222> LOCATION: (1)..(23)
182 <223> OTHER INFORMATION: Primer Sp6
185 <400> SEQUENCE: 11
186 tgaccacatc caaacatcct ctt                23
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190 <211> LENGTH: 25
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192 <213> ORGANISM: artificial sequence
194 <220> FEATURE:
195 <221> NAME/KEY: misc_feature
196 <222> LOCATION: (1)..(25)
197 <223> OTHER INFORMATION: Primer Sp5
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205 <211> LENGTH: 19
206 <212> TYPE: DNA
207 <213> ORGANISM: artificial sequence
209 <220> FEATURE:
210 <221> NAME/KEY: misc_feature
211 <222> LOCATION: (1)..(19)

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212 <223> OTHER INFORMATION: Primer Spep1
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219 <210> SEQ ID NO: 14
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221 <212> TYPE: DNA
222 <213> ORGANISM: Drosophila melanogaster
224 <220> FEATURE:
225 <221> NAME/KEY: CDS
226 <222> LOCATION: (1)..(6342)
227 <223> OTHER INFORMATION: CT28483
230 <400> SEQUENCE: 14
231 atg acc gcc tcg gat aaa tac acg tac cag cgg acc gtt ctc tgc ctg 48
232 Met Thr Ala Ser Asp Lys Tyr Thr Tyr Gln Arg Thr Val Leu Cys Leu
233 1 5 10 15
235 gcc cgc gtt ctg gcg ggc atc cag ccc act ccc tgg gat aag gta cat 96
236 Ala Arg Val Leu Ala Gly Ile Gln Pro Thr Pro Trp Asp Lys Val His
237 20 25 30
239 gtc cac ctg gcc acc cac tcc acc agc cac agc gcc agc ccc cct ggc 144
240 Val His Leu Ala Thr His Ser Thr Ser His Ser Ala Ser Pro Pro Gly
241 35 40 45
243 aat cga ctt ttc gca ctg acc ttg agc ggc ggc cat aaa aca gac atg 192
244 Asn Arg Leu Phe Ala Leu Thr Leu Ser Gly Gly His Lys Thr Asp Met
245 50 55 60
247 cgt ggg cgc tca ggg ggc ggc ggt aag gca gtg cag acc ctg ttc cgg 240
248 Arg Gly Arg Ser Gly Gly Gly Gly Lys Ala Val Gln Thr Leu Phe Arg
249 65 70 75 80
251 tat tgt ccg cag gag aat gct gcc gga gtg ttt tgc ctg gac acg cgg 288
252 Tyr Cys Pro Gln Glu Asn Ala Ala Gly Val Phe Cys Leu Asp Thr Arg
253 85 90 95
255 gcc cag gat gcc gta att gcg ctg ggc att tat ttt ctg gag ggc ggc 336
256 Ala Gln Asp Ala Val Ile Ala Leu Gly Ile Tyr Phe Leu Glu Gly Gly
257 100 105 110
259 tgc cag cac gag ggc cag att gtg ccc tat ctg ctg cgt ctg gcc aag 384
260 Cys Gln His Glu Gly Gln Ile Val Pro Tyr Leu Leu Arg Leu Ala Lys
261 115 120 125
263 tgt ctg ccg aag gcg gtc tgg att gac gat gcc cgg agc aac aaa gtg 432
264 Cys Leu Pro Lys Ala Val Trp Ile Asp Asp Ala Arg Ser Asn Lys Val
265 130 135 140
267 gaa cgc gtt cgc att ccg tcg gcg gaa aag ttc agc ttc tgc ttg aac 480
268 Glu Arg Val Arg Ile Pro Ser Ala Glu Lys Phe Ser Phe Cys Leu Asn
269 145 150 155 160
271 acc ctg ctg tcc gac ata gcg gcc aag tgt ccg gat tcg cgc gag gag 528
272 Thr Leu Leu Ser Asp Ile Ala Ala Lys Cys Pro Asp Ser Arg Glu Glu
273 165 170 175
275 atc atc ctg aat cag gtg gaa acg ctg agc gcg ctg gcc aac ata gtc 576
276 Ile Ile Leu Asn Gln Val Glu Thr Leu Ser Ala Leu Ala Asn Ile Val
277 180 185 190
279 aag tcg agc agg gac agc agc tcc gca ccg ccg ccc atc atc ctg tgc 624

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280	Lys	Ser	Ser	Arg	Asp	Ser	Ser	Ser	Ala	Pro	Pro	Pro	Ile	Ile	Leu	Cys	
281			195					200					205				
283	aag	gcc	acg	gtg	ccg	ctg	ctc	ttc	ggc	ttg	gcg	cga	tcg	atg	ggg	cgc	672
284	Lys	Ala	Thr	Val	Pro	Leu	Leu	Phe	Gly	Leu	Ala	Arg	Ser	Met	Gly	Arg	
285		210					215					220					
287	tat	gcc	agc	aac	gat	cca	ccg	ctg	ctg	tgc	cgc	att	ttt	ccg	ccc	gag	720
288	Tyr	Ala	Ser	Asn	Asp	Pro	Pro	Leu	Leu	Cys	Arg	Ile	Phe	Pro	Pro	Glu	
289	225					230					235					240	
291	ctg	ctg	ccc	atc	cag	aag	ggc	ggc	ggc	cgc	gac	ggc	acc	ggc	tcg	agc	768
292	Leu	Leu	Pro	Ile	Gln	Lys	Gly	Gly	Gly	Arg	Asp	Gly	Thr	Gly	Ser	Ser	
293					245					250						255	
295	agc	agt	gcc	agc	ggc	acc	tgc	ggc	ggc	tcc	ttc	agc	agc	agc	gaa	cgc	816
296	Ser	Ser	Ala	Ser	Gly	Thr	Cys	Gly	Gly	Ser	Phe	Ser	Ser	Ser	Glu	Arg	
297				260					265					270			
299	ctg	gcg	gcc	acg	cat	cac	ttc	cga	ccc	atc	ata	ccg	cgc	tcc	atg	tcc	864
300	Leu	Ala	Ala	Thr	His	His	Phe	Arg	Pro	Ile	Ile	Pro	Arg	Ser	Met	Ser	
301			275				280						285				
303	ggc	agt	ctg	gcg	cag	gcc	cag	aac	gca	agc	tac	gac	gat	gga	agg	cag	912
304	Gly	Ser	Leu	Ala	Gln	Ala	Gln	Asn	Ala	Ser	Tyr	Asp	Asp	Gly	Arg	Gln	
305		290					295					300					
307	cgg	tgc	gcg	ggc	ggc	aag	ccc	agc	aag	cca	tcg	ttg	cac	agc	tac	ttt	960
308	Arg	Cys	Ala	Gly	Gly	Lys	Pro	Ser	Lys	Pro	Ser	Leu	His	Ser	Tyr	Phe	
309	305					310					315					320	
311	tcg	gtg	ccg	tac	gat	ccg	cgg	acg	cac	ttc	ttc	acg	cgc	tac	ggc	tcc	1008
312	Ser	Val	Pro	Tyr	Asp	Pro	Arg	Thr	His	Phe	Phe	Thr	Arg	Tyr	Gly	Ser	
313					325					330						335	
315	agt	ttc	aac	caa	ttc	ccg	aac	atg	cgc	gtc	tgc	gaa	tcg	ccc	acg	aaa	1056
316	Ser	Phe	Asn	Gln	Phe	Pro	Asn	Met	Arg	Val	Cys	Glu	Ser	Pro	Thr	Lys	
317				340					345					350			
319	ggc	ggc	cca	cga	cca	ctg	tat	cgt	gtg	cct	ccg	ttt	ccc	atc	cag	cat	1104
320	Gly	Gly	Pro	Arg	Pro	Leu	Tyr	Arg	Val	Pro	Pro	Phe	Pro	Ile	Gln	His	
321			355				360							365			
323	cta	cag	acc	ata	ttc	gcg	gtg	tcc	aag	aag	ctg	ctc	acc	aaa	gac	acc	1152
324	Leu	Gln	Thr	Ile	Phe	Ala	Val	Ser	Lys	Lys	Leu	Leu	Thr	Lys	Asp	Thr	
325		370					375					380					
327	ctc	gaa	cat	ctc	gac	gag	cag	gca	agc	gat	ata	ttt	tcg	ctg	cac	caa	1200
328	Leu	Glu	His	Leu	Asp	Glu	Gln	Ala	Ser	Asp	Ile	Phe	Ser	Leu	His	Gln	
329	385					390					395					400	
331	atc	aag	ggc	tat	tgc	tac	aag	agc	ttc	tcg	gaa	acg	ttg	aac	ctg	gtc	1248
332	Ile	Lys	Gly	Tyr	Cys	Tyr	Lys	Ser	Phe	Ser	Glu	Thr	Leu	Asn	Leu	Val	
333				405						410						415	
335	ctg	gtg	acc	ctg	ctc	agg	gaa	ctg	ctg	cag	cat	cag	gtt	gac	ctg	ccc	1296
336	Leu	Val	Thr	Leu	Leu	Arg	Glu	Leu	Leu	Gln	His	Gln	Val	Asp	Leu	Pro	
337				420					425					430			
339	acg	ccg	ttc	acc	aag	gat	gtg	cag	gag	ttc	gtc	aag	cgg	ctc	ttt	ctc	1344
340	Thr	Pro	Phe	Thr	Lys	Asp	Val	Gln	Glu	Phe	Val	Lys	Arg	Leu	Phe	Leu	
341			435					440						445			
343	aac	ggc	caa	acg	gag	ctg	cag	aat	aaa	cag	cag	gat	cag	gaa	cgc	gag	1392
344	Asn	Gly	Gln	Thr	Glu	Leu	Gln	Asn	Lys	Gln	Gln	Asp	Gln	Glu	Arg	Glu	

RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:56; Xaa Pos. 415 ✓
Seq#:57; Xaa Pos. 415
Seq#:180; Xaa Pos. 551,572
Seq#:181; Xaa Pos. 551,572
Seq#:204; N Pos. 3000
Seq#:204; Xaa Pos. 1000
Seq#:205; Xaa Pos. 1000

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 9

VERIFICATION SUMMARY

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Input Set : N:\RJAVED\10527571.txt

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L:7030 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:56 after pos.:1248
L:7202 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:57 after pos.:400
L:27077 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:180 after pos.:1680
M:341 Repeated in SeqNo=180
L:27254 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:181 after pos.:544
M:341 Repeated in SeqNo=181
L:33762 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:204 after pos.:2976
M:341 Repeated in SeqNo=204
L:34028 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:205 after pos.:992